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RAW SEQUENCE LISTING                      DATE: 01/29/2001  
 PATENT APPLICATION: US/09/761,117        TIME: 13:47:07

Input Set : A:\43771apuy.app.txt  
 Output Set: N:\CRF3\01292001\I761117.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
 6     (i) APPLICANT: Dalla-Pavera, Riccardo  
 7                      Chaganti, Raju S.K.  
 9     (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
 10                      bcl-6  
 12     (iii) NUMBER OF SEQUENCES: 9  
 14     (iv) CORRESPONDENCE ADDRESS:  
 15             (A) ADDRESSEE: Cooper & Dunham LLP  
 16             (B) STREET: 1185 Avenue of the Americas  
 17             (C) CITY: New York  
 18             (D) STATE: New York  
 19             (E) COUNTRY: United States of America  
 20             (F) ZIP: 10036  
 22     (v) COMPUTER READABLE FORM:  
 23             (A) MEDIUM TYPE: Floppy disk  
 24             (B) COMPUTER: IBM PC compatible  
 25             (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 26             (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 28     (vi) CURRENT APPLICATION DATA:  
 C--> 29             (A) APPLICATION NUMBER: US/09/761,117  
 C--> 30             (B) FILING DATE: 16-Jan-2001  
 31             (C) CLASSIFICATION:  
 33     (vii) ATTORNEY/AGENT INFORMATION:  
 34             (A) NAME: White, John P.  
 35             (B) REGISTRATION NUMBER: 28,678  
 36             (C) REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y  
 38     (ix) TELECOMMUNICATION INFORMATION:  
 39             (A) TELEPHONE: (212) 278-0400  
 40             (B) TELEFAX: (212) 391-0525  
 41             (C) TELEX: 422523 COOP UI

Does Not Comply  
 Corrected Diskette Needed  
 See pp. 2-6

## ERRORED SEQUENCES

44 (2) INFORMATION FOR SEQ ID NO: 1:  
 46     (i) SEQUENCE CHARACTERISTICS:  
 47             (A) LENGTH: 3720 base pairs  
 48             (B) TYPE: nucleic acid  
 49             (C) STRANDEDNESS: double  
 50             (D) TOPOLOGY: linear  
 52     (ii) MOLECULE TYPE: cDNA  
 54     (ix) FEATURE:  
 55             (A) NAME/KEY: CDS  
 56             (B) LOCATION: 328..2445  
 58     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 E--> 60 GGCCCTCGA GCCTCGAACC GGAACCTCCA AATCCGAGAC GCTCTGCTTA

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```

61 TGAGGACCTC 60
E--> 63 GAAATATGCC GGCCAGTGAA AAAATCTTAT GGCTTTGAGG GCTTTTGTT
64 GGCCAGGGGC 120
E--> 66 AGTAAATC TCGGAGAGCT GACACCAAGT CCTCCCCTGC CACGTAGCAG
67 TGGTAAAGTC 180
E--> 69 CGAAGCTCAA ATCCGAGAA TTGAGCTCTG TTGATTCTTA GAATGGGGT
70 TCTTAGAAGT 240
E--> 72 GGTGATGCAA GAAGTTTCTA GGAAGGCCG GACACCAGGT TTTAGCAAA
73 ATTTTGGACT 300
E--> 75 GTGAAGCAAG GCATTGGTGA AGACAAA ATG GCC TCG CCG GCT GAC AGC TGT
W--> 76 351
77 Met Ala Ser Pro Ala Asp Ser Cys
78 1 5
E--> 80 ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT AAT CGT
W--> 81 399
82 Ile Gln Phe Thr Arg His Ala Arg Asp Val Leu Leu Asn Leu Asn Arg
W--> 83 10 15 20
E--> 85 CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT
W--> 86 447
87 Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg
W--> 88 25 30 35 40
E--> 90 GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GGC CTG
W--> 91 495
92 Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Trp Arg Gly Leu
W--> 93 45 50 55
E--> 95 TTC TAT AGC ATC TTT ACA GAC CAG TTG AAA TGC AAC CTT AGT GTG ATC
W--> 96 543
97 Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile
W--> 98 60 65 70
E--> 100 AAT CTA GAT CCT GAG ATC AAC CCT GAG GGA TTC TGC ATC CTC CTG GAC
W--> 101 591
102 Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp
W--> 103 75 80 85
E--> 105 TTC ATG TAC ACA TCT CGG CTC AAT TTG CGG GAG GGC AAC ATC ATG GCT
W--> 106 639
107 Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala
W--> 108 90 95 100
E--> 110 GTG ATG GCC ACG GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT
W--> 111 687
112 Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr
W--> 113 105 110 115 120
E--> 115 TGC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC
W--> 116 735
117 Cys Arg Lys Phe Ile Lys Ala Ser Glu Ala Glu Met Val Ser Ala Ile
W--> 118 125 130 135
E--> 120 AAG CCT CCT CGT GAA GAG TTC CTC AAC AGC CGG ATG CTG ATG CCC CAA
W--> 121 783
122 Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln
W--> 123 140 145 150

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Wrapped nucleic acids. The text or numbers have "wrapped" down to the next line.

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```

E--> 125 GAC ATC ATG GCC TAT CGG GGT CGT GAG GTG GTG GAG AAC AAC CTG CCA
W--> 126 831
      127 Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Leu Pro
      155 160 165
W--> 128
E--> 130 CTG AGG AGC GCC CCT GGG TGT GAG AGC AGA GCC TTT GCC CCC AGC CTG
W--> 131 879
      132 Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu
      170 175 180
W--> 133
E--> 135 TAC AGT GGC CTG TCC ACA CCG CCA GCC TCT TAT TCC ATG TAC AGC CAC
W--> 136 927
      137 Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His
      190 195 200
W--> 138 185
E--> 140 CTC CCT GTC AGC AGC CTC CTC TTC TCC GAT GAG GAG TTT CGG GAT GTC
W--> 141 975
      142 Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val
      205 210 215
W--> 143
E--> 145 CGG ATG CCT GTG GCC AAC CCC TTC CCC AAG GAG CGG GCA CTC CCA TGT
W--> 146 1023
      147 Arg Met Pro Val Ala Asn Pro Phe Pro Lys Glu Arg Ala Leu Pro Cys
      220 225 230
W--> 148
E--> 150 GAT AGT GCC AGG CCA GTC CCT GGT GAG TAC AGC CGG CCG ACT TTG GAG
W--> 151 1071
      152 Asp Ser Ala Arg Pro Val Pro Gly Glu Tyr Ser Arg Pro Thr Leu Glu
      235 240 245
W--> 153
E--> 155 GTG TCC CCC AAT GTG TGC CAC AGC AAT ATC TAT TCA CCC AAG GAA ACA
W--> 156 1119
      157 Val Ser Pro Asn Val Cys His Ser Asn Ile Tyr Ser Pro Lys Glu Thr
      250 255 260
W--> 158
E--> 160 ATC CCA GAA GAG GCA CGA AGT GAT ATG CAC TAC AGT GTG GCT GAG GGC
W--> 161 1167
      162 Ile Pro Glu Glu Ala Arg Ser Asp Met His Tyr Ser Val Ala Glu Gly
      270 275 280
W--> 163 265
E--> 165 CTC AAA CCT GCT GCC CCC TCA GCC CGA AAT GCC CCC TAC TTC CCT TGT
W--> 166 1215
      167 Leu Lys Pro Ala Ala Pro Ser Ala Arg Asn Ala Pro Tyr Phe Pro Cys
      285 290 295
W--> 168
E--> 170 GAC AAG GCC AGC AAA GAA GAG AGA CCC TCC TCG GAA GAT GAG ATT
W--> 171 1263
      172 Asp Lys Ala Ser Lys Glu Glu Glu Arg Pro Ser Ser Glu Asp Glu Ile
      300 305 310
W--> 173
E--> 175 GCC CTG CAT TTC GAG CCC CCC AAT GCA CCC CTG AAC CGG AAG GGT CTG
W--> 176 1311
      177 Ala Leu His Phe Glu Pro Pro Asn Ala Pro Leu Asn Arg Lys Gly Leu
      315 320 325
W--> 178
E--> 180 GTT AGT CCA CAG AGC CCC CAG AAA TCT GAC TGC CAG CCC AAC TCG CCC
W--> 181 1359
      182 Val Ser Pro Gln Ser Pro Gln Lys Ser Asp Cys Gln Pro Asn Ser Pro
      330 335 340
W--> 183
E--> 185 ACA GAG GCC TGC AGC AGT AAG AAT GCC TGC ATC CTC CAG GGT TCT GGC

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```

W--> 186 1407
      187 Thr Glu Ala Cys Ser Ser Lys Asn Ala Cys Ile Leu Gln Gly Ser Gly
      350 355 360
W--> 188 345
E--> 190 TCC CCT CCA GCC AAG AGC CCC ACT GAC CCC AAA GCC TGC AGC TGG AAG
W--> 191 1455
      192 Ser Pro Pro Ala Lys Ser Pro Thr Asp Pro Lys Ala Cys Ser Trp Lys
      365 370 375
W--> 193
E--> 195 AAA TAC AAG TTC ATC GTG CTC AAC AGC CTC AAC CAG AAT GCC AAA CCA
W--> 196 1503
      197 Lys Tyr Lys Phe Ile Val Leu Asn Ser Leu Asn Gln Asn Ala Lys Pro
      380 385 390
W--> 198
E--> 200 GGG GGG CCT GAG CAG GCT GAG CTG GGC CGC CTT TCC CCA CGA GCC TAC
W--> 201 1551
      202 Gly Gly Pro Glu Gln Ala Glu Leu Gly Arg Leu Ser Pro Arg Ala Tyr
      395 400 405
W--> 203
E--> 205 ACG GCC CCA CCT GCC TGC CAG CCA CCC ATG GAG CCT GAG AAC CTT GAC
W--> 206 1599
      207 Thr Ala Pro Pro Ala Cys Gln Pro Pro Met Glu Pro Glu Asn Leu Asp
      410 415 420
W--> 208
E--> 210 CTC CAG TCC CCA ACC AAG CTG AGT GCC AGC GGG GAG GAC TCC ACC ATC
W--> 211 1647
      212 Leu Gln Ser Pro Thr Lys Leu Ser Ala Ser Gly Glu Asp Ser Thr Ile
      430 435 440
W--> 213 425
E--> 215 CCA CAA GCC AGC CGG CTC AAT AAC ATC GTT AAC AGG TCC ATG ACG GGC
W--> 216 1695
      217 Pro Gln Ala Ser Arg Leu Asn Asn Ile Val Asn Arg Ser Met Thr Gly
      445 450 455
W--> 218
E--> 220 TCT CCC CGC AGC AGC AGC GAG AGC CAC TCA CCA CTC TAC ATG CAC CCC
W--> 221 1743
      222 Ser Pro Arg Ser Ser Ser Glu Ser His Ser Pro Leu Tyr Met His Pro
      460 465 470
W--> 223
E--> 225 CCG AAG TGC ACG TCC TGC GGC TCT CAG TCC CCA CAG CAT GCA GAG ATG
W--> 226 1791
      227 Pro Lys Cys Thr Ser Cys Gly Ser Gln Ser Pro Gln His Ala Glu Met
      475 480 485
W--> 228
E--> 230 TGC CTC CAC ACC GCT GGC CCC ACG TTC GCT GAG GAG ATG GGA GAG ACC
W--> 231 1839
      232 Cys Leu His Thr Ala Gly Pro Thr Phe Ala Glu Glu Met Gly Glu Thr
      490 495 500
W--> 233
E--> 235 CAG TCT GAG TAC TCA GAT TCT AGC TGT GAG AAC GGG GCC TTC TTC TGC
W--> 236 1887
      237 Gln Ser Glu Tyr Ser Asp Ser Ser Cys Glu Asn Gly Ala Phe Phe Cys
      510 515 520
W--> 238 505
E--> 240 AAT GAG TGT GAC TGC CGC TTC TCT GAG GAG GCC TCA CTC AAG AGG CAC
W--> 241 1935
      242 Asn Glu Cys Asp Cys Arg Phe Ser Glu Glu Ala Ser Leu Lys Arg His
      525 530 535
W--> 243
E--> 245 ACG CTG CAG ACC CAC AGT GAC AAA CCC TAC AAG TGT GAC CGC TGC CAG
W--> 246 1983

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1/29/01

file://C:\CRF3\Outhold\VsrI761117.htm

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```

247 Thr Leu Gln Thr His Ser Asp Lys Pro Tyr Lys Cys Asp Arg Cys Gln
W--> 248          540          545          550
E--> 250 GCC TCC TTC CGC TAC AAG GGC AAC CTC GCC AGC CAC AAG ACC GTC CAT
W--> 251 2031
252 Ala Ser Phe Arg Tyr Lys Gly Asn Leu Ala Ser His Lys Thr Val His
W--> 253          555          560          565
E--> 255 ACC GGT GAG AAA CCC TAT CGT TGC AAC ATC TGT GGG GCC CAG TTC AAC
W--> 256 2079
257 Thr Gly Glu Lys Pro Tyr Arg Cys Asn Ile Cys Gly Ala Gln Phe Asn
W--> 258          570          575          580
E--> 260 CGG CCA GCC AAC CTG AAA ACC CAC ACT CGA ATT CAC TCT GGA GAG AAG
W--> 261 2127
262 Arg Pro Ala Asn Leu Lys Thr His Thr Arg Ile His Ser Gly Glu Lys
W--> 263 585          590          595          600
E--> 265 CCC TAC AAA TGC GAA ACC TGC GGA GCC AGA TTT GTA CAG GTG GCC CAC
W--> 266 2175
267 Pro Tyr Lys Cys Glu Thr Cys Gly Ala Arg Phe Val Gln Val Ala His
W--> 268          605          610          615
E--> 270 CTC CGT GCC CAT GTG CTT ATC CAC ACT GGT GAG AAG CCC TAT CCC TGT
W--> 271 2223
272 Leu Arg Ala His Val Leu Ile His Thr Gly Glu Lys Pro Tyr Pro Cys
W--> 273          620          625          630
E--> 275 GAA ATC TGT GGC ACC CGT TTC CGG CAC CTT CAG ACT CTG AAG AGC CAC
W--> 276 2271
277 Glu Ile Cys Gly Thr Arg Phe Arg His Leu Gln Thr Leu Lys Ser His
W--> 278          635          640          645
E--> 280 CTG CGA ATC CAC ACA GGA GAG AAA CCT TAC CAT TGT GAG AAG TGT AAC
W--> 281 2319
282 Leu Arg Ile His Thr Gly Glu Lys Pro Tyr His Cys Glu Lys Cys Asn
W--> 283          650          655          660
E--> 285 CTG CAT TTC CGT CAC AAA AGC CAG CTG CGA CTT CAC TTG CGC CAG AAG
W--> 286 2367
287 Leu His Phe Arg His Lys Ser Gln Leu Arg Leu His Leu Arg Gln Lys
W--> 288 665          670          675          680
E--> 290 CAT GGC GCC ATC ACC AAC ACC AAG GTG CAA TAC CGC GTG TCA GCC ACT
W--> 291 2415
292 His Gly Ala Ile Thr Asn Thr Lys Val Gln Tyr Arg Val Ser Ala Thr
W--> 293          685          690          695
E--> 295 GAC CTG CCT CCG GAG CTC CCC AAA GCC TGC TGAAGCATGG AGTGTGTGATG
W--> 296 2465
297 Asp Leu Pro Pro Glu Leu Pro Lys Ala Cys
W--> 298          700          705
E--> 300 CTTTCGTCTC CAGCCCCCTC TCAGAATCTA CCCAAAGGAT ACTGTAACAC
301 TTACCAATGT 2525
E--> 303 TCATCCCATG ATGTAGTGCC TCTTTCATCC ACTAGTGCAA ATCATAGCTG
304 GGGGTGTTGGG 2585
E--> 306 GTGGTGGGGG TCGGGGCCCTG GGGGACTGGG AGCCGCAGCA GCTCCCCCTC
307 CCCCCTGCC 2645
E--> 309 ATAAACATT AAGAAATCA TATTGCTTCT TCTCCTATGT GNNNNNNNNN

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Input Set : A:\43771apuy.app.txt  
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310 NNNNNNNNNN 2705  
E--> 312 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
313 NNNNNNNNNN 2765  
E--> 315 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
316 NNNNNNNNNN 2825  
E--> 318 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
319 NNNNNNNNNN 2885  
E--> 321 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
322 NNNNNNNNNN 2945  
E--> 324 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
325 NNNNNNNNNN 3005  
E--> 327 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
328 NNNNNNNNNN 3065  
E--> 330 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
331 NNNNNNNNNN 3125  
E--> 333 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
334 NNNNNNNNNN 3185  
E--> 336 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
337 NNNNNNNNNN 3245  
E--> 339 NTTAAGTAT TGCATCTGTA TAAGTAAGAA AATATTTTGT CTAAATGCC  
340 TCAGTGTATT 3305  
E--> 342 TGTATTTTTT TGCAAGTGGG GGGTACAAT TTACCCAGTG TGTATTA  
343 AAAACCCAAA 3365  
E--> 345 GAACCCAAAA ATCTCCAGAA GGAAAAATGT GTAATTTTGT TCTAGTTTT  
346 AGTTTGTATA 3425  
E--> 348 TACCCGTACA ACGTGTCTC ACGGTGCCTT TTTTCACGGA AGTTTCAAT  
349 GATGGCGGAG 3485  
E--> 351 CGTGACCAT CCCTTTTGA AGTGTAGGCA GACACAGGGA CTGAAGTTG  
352 TTAATACTA 3545  
E--> 354 AACTCTCTTT GGAATGTTT GTCTCATCCC ANCTGCGTC ATGCTGTGT  
355 GATACTACT 3605  
E--> 357 CCGGAGACAG GGTTCGCTG TGTCTAACT GCATTACCGC GTTGTA  
358 ATAGCTGTAC 3665  
E--> 360 CAATATAAGA ATAAATGTT GGAAAGTCGC AAAAAAAAAA AAAAAAAAAA  
361 AAAAA 3720

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/761,117

DATE: 01/29/2001  
TIME: 13:47:08

Input Set : A:\4377lapuy.app.txt  
Output Set: N:\CRF3\01292001\I761117.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:60 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1  
M:254 Repeated in SeqNo=1  
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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Input Set : A:\4377lapuy.app.txt  
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L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1